IN THE CLAIMS

Please cancel Claim 20 without prejudice or disclaimer of the subject matter therein.

Please amend the claims as follows:

1. (Previously presented) An isolated mutant IgE protein, wherein mutant IgE_{HC} proteins of said mutant IgE protein have reduced spatial mobility compared to the spatial mobility of unmodified IgE_{HC} proteins in an unmodified IgE protein, wherein said unmodified IgE_{HC}'s comprise the amino acid sequence of SEQ ID NO:11.

2. (Previously presented) The isolated mutant IgE protein of Claim 1, wherein said mutant IgE protein is constrained to the open conformation or the closed conformation.

3. (Previously presented) The isolated mutant IgE protein of Claim 1, wherein the N-terminal amino-acids residues of the Cϵ3 domains of said mutant IgE_{HC} proteins are unable to obtain an inter-residue distance of 23Å or more.

4. (Previously presented) The isolated mutant IgE protein of Claim 1, wherein the N-terminal amino-acids residues of the Cϵ3 domains of said mutant IgE_{HC} proteins have a fixed, inter-residue distance of between about 13 Å and less than 23 Å.

5. (Previously presented) The isolated mutant IgE protein of Claim 1, wherein said mutant IgE protein is constrained in a conformation in which the N-terminal amino-acids residues of the Cϵ3 domains of said IgE_{HC} proteins have an inter-residue distance selected from the group consisting of a distance of about 13Å, a distance of about 14Å, a distance of about 15Å, a distance of about 16Å, a distance of about 17Å, a distance of about 18Å, a distance of about 19Å, a distance of about 20Å, a distance of about 21Å a distance of about 22Å or a distance of between about 22 Å and less than 23Å.

6. (Previously presented) The isolated mutant IgE protein of Claim 1, wherein said mutant IgE protein comprises a IgE_{HC} protein that comprises an amino acid sequence at least about 80% identical to SEQ ID NO:11, wherein the amino acid in said protein corresponding to position 2, 3, 4, 5, 6, 7, 8 or 9 or SEQ ID NO:11 is a cysteine or methionine.

7. (Previously presented) The isolated mutant IgE protein of Claim 6, wherein said mutant IgE protein binds to an antibody raised against an IgE protein comprising an unmodified IgE_{HC} comprising the amino acid sequence of SEQ ID NO:11.

8. (Previously presented) The isolated mutant IgE protein of Claim 1, wherein said mutant IgE_{HC} proteins comprise an amino acid sequence selected from the group consisting of SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:27.

9. (Previously presented) An isolated nucleic acid molecule comprising a nucleic acid sequence at least about 80% identical to SEQ ID NO:10, wherein the codon in said nucleic acid sequence corresponding to nucleotides 4-6, 7-9, 10-12, 13-15, 16-18, 19-21, 22-24, or 25-27 of SEQ ID NO:10 encodes a cysteine or a methionine.

10. (Previously presented) The isolated nucleic acid molecule of Claim 9, wherein said nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of:

(a) a nucleic acid sequence at least about 90% identical to SEQ ID NO:10, wherein the codon at nucleotides 4-6 of said nucleic acid sequence encodes a cysteine or a methionine;

(b) a nucleic acid sequence at least about 90% identical to SEQ ID NO:10, wherein the codon at nucleotides 7-9 of said nucleic acid sequence encodes a cysteine or a methionine;

(c) a nucleic acid sequence at least about 90% identical to SEQ ID NO:10, wherein the codon at nucleotides 10-12 of said nucleic acid sequence encodes a cysteine or a methionine;

(d) a nucleic acid sequence at least about 90% identical to SEQ ID NO:10, wherein the codon at nucleotides 13-15 of said nucleic acid sequence encodes a cysteine or a methionine;

(e) a nucleic acid sequence at least about 90% identical to SEQ ID NO:10, wherein the codon at nucleotides 16-18 of said nucleic acid sequence encodes a cysteine or a methionine;

(f) a nucleic acid sequence at least about 90% identical to SEQ ID NO:10, wherein the codon at nucleotides 19-21 of said nucleic acid sequence encodes a cysteine or a methionine;

(g) a nucleic acid sequence at least about 90% identical to SEQ ID NO:10, wherein the codon at nucleotides 22-24 of said nucleic acid sequence encodes a cysteine or a methionine; and

(h) a nucleic acid sequence at least about 90% identical to SEQ ID NO:10, wherein the codon at nucleotides 25-27 of said nucleic acid sequence encodes a cysteine or a methionine.

11. (Previously presented) The isolated nucleic acid molecule of Claim 9, wherein said nucleic acid sequence encodes a protein having an amino acid sequence at least about 80% identical to SEQ ID NO:11, wherein the amino acid in said protein corresponding to position 2, 3, 4, 5, 6, 7, 8 or 9 or SEQ ID NO:11 is a cysteine or methionine and wherein said protein binds an antibody raised against a protein having the amino acid sequence of SEQ ID NO:11.

12. (Previously presented) The isolated nucleic acid molecule of Claim 9, wherein said nucleic acid sequence is selected from the group consisting of SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24 and SEQ ID NO:26.

13. (Previously presented) An isolated protein having an amino acid sequence at least about 80% identical to SEQ ID NO:11, wherein the amino acid in said protein corresponding to position 2, 3, 4, 5, 6, 7, 8 or 9 or SEQ ID NO:11 is a cysteine or methionine and wherein said protein binds to an antibody raised against a protein having the amino acid sequence of SEQ ID NO:11.

14. (Previously presented) The isolated protein of Claim 13, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence at least about 90% identical to SEQ ID NO:11, wherein the amino acid at position 2 of such amino acid sequence is a cysteine or a methionine;

(b) an amino acid sequence at least about 90% identical to SEQ ID NO:11, wherein the amino acid at position 3 of such amino acid sequence is a cysteine or a methionine;

(c) an amino acid sequence at least about 90% identical to SEQ ID NO:11, wherein the amino acid at position 4 of such amino acid sequence is a cysteine or a methionine;

(d) an amino acid sequence at least about 90% identical to SEQ ID NO:11, wherein the amino acid at position 5 of such amino acid sequence is a cysteine or a methionine;

(e) an amino acid sequence at least about 90% identical to SEQ ID NO:11, wherein the amino acid at position 6 of such amino acid sequence is a cysteine or a methionine;

(f) an amino acid sequence at least about 90% identical to SEQ ID NO:11, wherein the amino acid at position 7 of such amino acid sequence is a cysteine or a methionine;

(g) an amino acid sequence at least about 90% identical to SEQ ID NO:11, wherein the amino acid at position 8 of such amino acid sequence is a cysteine or a methionine; and

(h) an amino acid sequence at least about 90% identical to SEQ ID NO:11, wherein the amino acid at position 9 of such amino acid sequence is a cysteine or a methionine.

15. (Previously presented) The isolated protein of Claim 13, wherein said protein comprises an amino acid sequence selected from SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:17.

16. (Currently amended) A method selected from the group consisting of:

(a) a method to identify a compound that inhibits the binding of IgE to a FcεRI, said method comprising:

(i) contacting an isolated mutant IgE protein of Claim 1 ~~or an isolated protein of Claim 13~~ with a putative inhibitory compound in the presence of a FcεRI or FcεRIα protein; and

(ii) determining if said putative inhibitory compound inhibits the binding of said mutant IgE protein of Claim 1 ~~or said isolated protein of Claim 13~~ to said FcεRI or FcεRIα protein; ~~and~~

(b) a method to identify a compound that binds to IgE ~~either~~ ~~in or~~ ~~resulting~~ in a closed conformation, said method comprising:

(i) contacting an isolated mutant IgE protein of Claim 1 ~~or an isolated protein of Claim 13~~ with a putative inhibitory compound in the presence of a FcεRI or FcεRIα protein; and

(ii) determining if said putative inhibitory compound binds to said mutant IgE protein of Claim 1 ~~or said isolated protein of Claim 13~~ ; and

(c) a method to identify a compound that causes IgE to adopt a closed conformation, said method comprising:

(i) contacting an isolated IgE protein with a putative inhibitory compound; and

(ii) determining if said putative inhibitory causes said IgE protein to adopt a closed conformation.

17. (Previously presented) The method of Claim 16, wherein said mutated IgE molecule comprises IgE_{HC}'s comprising an amino acid sequence at least about 90% identical to SEQ ID NO:11, wherein the amino acid in said protein corresponding to position 2,3 ,4, 5, 6, 7, 8 or 9 or SEQ ID NO:11 is a cysteine or methionine and wherein said protein binds an antibody raised against a protein having the amino acid sequence of SEQ ID NO:11.

18. (Previously presented) An isolated compound that inhibits the binding of IgE to an FcεRI, wherein said compound is identified by the method of Claim 16.

19. (Previously presented) The isolated compound of Claim 18, wherein said compound does not bind the open form of IgE.

20. (Canceled)

21. (Currently amended) A method to protect an animal from a disease mediated by IgE, said method comprising administering a composition of Claim ~~20~~ 18.

22. (Currently amended) A kit comprising an isolated mutant IgE protein of Claim 1 ~~or an isolated protein of Claim 13~~ and a means to determine if a compound binds to said isolated mutant IgE protein of Claim 1 ~~or said isolated protein of Claim 13~~.